

SEQUENCE LISTING

<110> Taylor, Alexander H

<120> Monoclonal Antibodies with Reduced
Immunogenicity

<130> P50770

<150> 60/083,367

<151> 1998-04-28

<160> 97

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

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5

10

15

gtc ctg tcc cag gtg cag ttg cag gag tcg ggc cca gga ctg gtg aag 96

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys

20

25

30

cct tca cag acc ttg tcc ctg acc tgc gct gtg tct ggt ggc tcc atc 144

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile

35

40

45

act agt gct tac tac tat tgg agc tgg atc cgc cag tca cca ggg aag 192
 Thr Ser Ala Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys

50

55

60

gga ctg gag tgg att ggg agt atc tat tat agt ggg acc att ttc tcc 240
 Gly Leu Glu Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser
 65 70 75 80

aac cca tcc ctc aag agt cga gtc gcc atg tca gta ggc acg tcc aag 288
 Asn Pro Ser Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys
 85 90 95

acc cag ttc tcc ctg agc ttg agt tct gtg acc gcc gcg gac acg gcc 336
 Thr Gln Phe Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110

gtg tac tac tgt gcg aga ggt ctg ctc ctc acc att gga ctg acc aac 384
 Val Tyr Tyr Cys Ala Arg Gly Leu Leu Leu Thr Ile Gly Leu Thr Asn
 115 120 125

tac tac ttt gac tac tgg ggc ccg gga acc ctg gtc acc gtc ttc 429
 Tyr Tyr Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val Thr Val Phe
 130 135 140

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
gtc ctg tcc cag gtg cag cta cag gag tcg ggc cca gga cta gtg aag	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
ccg tca cag acc ctg tcc ctc acc tgc ggt gtc tct ggt gcc tcc atc	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile	
35 40 45	
aat agt ggt gtt cat tac tgg gcc tgg ata cgc cag cct gca gga aag	192
Asn Ser Gly Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys	
50 55 60	
gga ctg gag tgg att ggc aat atc tat cat agt ggg agc gcc tac tac	240
Gly Leu Glu Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr	
65 70 75 80	
act cca tcc ctc gag agt cga gtc tcc atg tca ata gag acg tcc aag	288
Thr Pro Ser Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys	
85 90 95	
agc cag ttc ttc cta aac tta aat tct ctg acc gcc gcg gac acg gct	336
Ser Gln Phe Phe Leu Asn Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala	
100 105 110	
atc tat tat tgt gcg aga cga cat act tcg tca gac tac ttt gac ttt	384
Ile Tyr Tyr Cys Ala Arg Arg His Thr Ser Ser Asp Tyr Phe Asp Phe	
115 120 125	
tgg ggc cgc gga atc ctg gtc atc gtc tcc	414
Trp Gly Arg Gly Ile Leu Val Ile Val Ser	
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<220>
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gtc cgt gca gac gtg cag ctg gtg cag tcc gga gca gag gtg aaa aag 96
 Val Arg Ala Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

ccc ggg gag tct ctg aag atc tcc tgt aag gtc tct gga aat gaa ttt 144
 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe
 35 40 45

acc aac tac tgg atc gcc tgg gtg cgc cag atg tcc ggg aaa ggc ctg 192
 Thr Asn Tyr Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu
 50 55 60

gag tgg atg ggg agc atc tat cct ggt gac tct gat acc aga tac aac 240
 Glu Trp Met Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn
 65 70 75 80

ccg tcc ttc caa ggc caa gtc acc ttt tca gcc gac aag tcc atc acc 288
 Pro Ser Phe Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr
 85 90 95

acc gcc tat ttg cag tgg agt agt ctg gag gcc tcg gac acc gcc atg 336
 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met
 100 105 110

tac tac tgt gcg agc cga aat cac ttt gtt ttc ggg gaa gtt att act	384		
Tyr Tyr Cys Ala Ser Arg Asn His Phe Val Phe Gly Glu Val Ile Thr			
115	120	125	
act ttg acg gct ggg gcc agg gaa acc ctg ggt cac cgt ctc c	427		
Thr Leu Thr Ala Gly Ala Arg Glu Thr Leu Gly His Arg Leu			
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Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly Val Gln			
1	5	10	15
tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg	96		
Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly			
20	25	30	
ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc agt agg	144		
Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg			
35	40	45	
agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg ggg tgg	192		
Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp			
50	55	60	
ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg gac tca	240		

Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser Asp Ser				
65	70	75	80	
				288
gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat tca ctc				
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu				
85	90	95		
				336
tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt tat tac				
Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe Tyr Tyr				
100	105	110		
				384
tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc cag gga				
Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly Gln Gly				
115	120	125		
				402
acc ctg gtc acc gtc tcc				
Thr Leu Val Thr Val Ser				
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Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly				
1	5	10	15	
gtc cag tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag				
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln				
20	25	30		

cct	ggg	ggg	tcc	ttg	aca	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	144
Pro	Gly	Gly	Ser	Leu	Thr	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	
35															45	
agt	agg	agt	ggc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggg	aag	gga	ctg	192
Ser	Arg	Ser	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
50															60	
gag	tgg	ctt	gca	tac	att	gat	tat	ggc	agt	att	ttc	ata	tac	tac	tcg	240
Glu	Trp	Leu	Ala	Tyr	Ile	Asp	Tyr	Gly	Ser	Ile	Phe	Ile	Tyr	Tyr	Ser	
65															80	
gac	tca	gtg	aag	ggc	cgc	ttc	acc	atc	tcc	aga	gac	aac	gcc	aag	aat	288
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
85															95	
tca	ctc	tat	ctg	caa	atg	aac	agc	ctg	aga	gcc	gac	gac	acg	gct	ttt	336
Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Phe	
100															110	
tat	tac	tgt	acg	acc	cat	aat	tgg	ggg	gag	tta	act	gac	tac	tgg	ggc	384
Tyr	Tyr	Cys	Thr	Thr	His	Asn	Trp	Gly	Glu	Leu	Thr	Asp	Tyr	Trp	Gly	
115															125	
ca g	gga	acc	ctg	gtc	acc	gtc	tcc									408
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser									
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<211> 421

<212> DNA

<213> Pan troglodytes

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<222> (1)...(421)

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1 5 10 15	
gga gtc tgt gca gag gtg cag ctg gtg cag tct gga gca gag gtg aaa	96
Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys	
20 25 30	
aag ccc ggg gag tct ctg aag atc tcc tgt aag ggc tct gga tac agt	144
Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser	
35 40 45	
ttt acc aac tac tgg atg ggc tgg gtg tgc cag atg ccc ggg aaa ggc	192
Phe Thr Asn Tyr Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly	
50 55 60	
ccg gag tgc atg ggg atc atc tat cct gat gac tct gat acc aga tac	240
Pro Glu Cys Met Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr	
65 70 75 80	
agc ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc	288
Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile	
85 90 95	
agc acc gcc tac cta caa tgg agc aac ctg aag gcc tcg gac acc gcc	336
Ser Thr Ala Tyr Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala	
100 105 110	
ata tat tac tgt gcg aga tgt tat ggt act act tgc gaa gct ttt	384
Ile Tyr Tyr Cys Ala Arg Cys Tyr Gly Trp Thr Thr Cys Glu Ala Phe	
115 120 125	
gat atc tgg ggc caa ggg aca atg gtc acc gtc tct t	421
Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser	

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<210> 7

<211> 417

<212> DNA

<213> Pan troglodytes

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 Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
 1 5 10 15

cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tca cag
 Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 20 25 30

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
 35 40 45

agt tac tac tgg agt tgg atc cgg cag ccc gcc ggg aag cga ctg gag
 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu
 50 55 60

tgg att ggg tat att tat tat agt ggg agt acc tac aac cca tcc
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 65 70 75 80

ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttc
 Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
 85 90 95

tcc ctg aag ctg agc tct gtg acc gcc gca gac acg gcc gtc tat tac	336		
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr			
100	105	110	
tgt gcg aga tct ccc caa aac gta tta caa tct ttg gac tgc ttc gac	384		
Cys Ala Arg Ser Pro Gln Asn Val Leu Gln Ser Leu Asp Cys Phe Asp			
115	120	125	
ccc tgg ggc cag gga acc ctg gtc acc gtc tcc	417		
Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser			
130	135		
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Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
1	5	10	15
cct ggg tcc tca gtg aag gtc tcc tgc aag gtt tcc gga ggc acc ttc	96		
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe			
20	25	30	
agc acc tat ggt ttc agc tgg gtg cgg cag gcc cct gga caa ggg ctt	144		
Ser Thr Tyr Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
35	40	45	
gag tgg atg gga atg atc atc cct atc gtt ggc aca gta aag tac gca	192		
Glu Trp Met Gly Met Ile Ile Pro Ile Val Gly Thr Val Lys Tyr Ala			

50

55

60

cag agg ttc cag ggc aga gtc tca att aat gcg gac aca tcc acg aat 240
 Gln Arg Phe Gln Gly Arg Val Ser Ile Asn Ala Asp Thr Ser Thr Asn

65

70

75

80

ata gcc tac atg gag ctg acc agc ctg aga tct gag gac acg gcc gtc 288
 Ile Ala Tyr Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val

85

90

95

tat tac tgt gcg aca gat ctg acg gtg act act aat gat gca ttt gat 336
 Tyr Tyr Cys Ala Thr Asp Leu Thr Val Thr Thr Asn Asp Ala Phe Asp

100

105

110

atc tgg ggc caa ggg aca atg gtc acc gtc tct 369
 Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser

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120

<210> 9

<211> 423

<212> DNA

<213> Pan troglodytes

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<221> CDS

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 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

1

5

10

15

gtc cag tgt gag gtg cag ctg gtg gag tct ggg gaa ggc ttg gta aag 96
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Glu Gly Leu Val Lys

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25

30

cct ggg ggt tcc ctg aga ctc tcg tgt gca gcc tct gga ttc acc ttc 144
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35

40

45

- -agt agt ttt ctt atg ttc tgg gtc cgc cag gct cca gaa aag ggg ctg 192
 Ser Ser Phe Leu Met Phe Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
 50 55 60

gag tgg gtc tca act att gat gtt agt ggt ggt aat atg tgg tac cga 240
 Glu Trp Val Ser Thr Ile Asp Val Ser Gly Gly Asn Met Trp Tyr Arg
 65 70 75 80

gac tct gtc aag ggc cga ttc acc atg tcc aga gac aat tcc aag aac 288
 Asp Ser Val Lys Gly Arg Phe Thr Met Ser Arg Asp Asn Ser Lys Asn
 85 90 95

aca ctg tat ctg caa atg acc agc ctg aga gcc gac gac acg gcc gtt 336
 Thr Leu Tyr Leu Gln Met Thr Ser Leu Arg Ala Asp Asp Thr Ala Val
 100 105 110

tac tat tgt gcg aga gag gga cga gac cct agc ggc act tgg gga tac 384
 Tyr Tyr Cys Ala Arg Glu Gly Arg Asp Pro Ser Gly Thr Trp Gly Tyr
 115 120 125

ttt gac tac tgg ggc cag gga atc ctg gtc acc gtc tcc 423
 Phe Asp Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser
 130 135 140

<210> 10

<211> 97

<212> PRT

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<222> (31)...(37)

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<221> DOMAIN

<222> (52) . . . (67)

<223> CDRII

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Thr Ser Ala

20 25 30

Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys Thr Gln Phe

65 70 75 80

Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys

<210> 11

<211> 96

<212> PRT

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- - - - - <220> - - - - -

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<222> (31) . . . (37)

<223> CDRI

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<223> CDRII

<400> 11

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile Asn Ser Gly
 20 25 30
 Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu
 35 40 45
 Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr Thr Pro Ser
 50 55 60
 Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys Ser Gln Phe
 65 70 75 80
 Phe Leu Asn Leu Asn Ser Leu Thr Ala Asp Thr Ala Ile Tyr Tyr Cys
 85 90 95

<210> 12

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<222> (50)...(66)

<223> CDRII

<400> 12

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe Thr Asn Tyr
 20 25 30
 Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr

65	70	75	80
Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met Tyr Tyr Cys			
85	90	95	

<210> 13

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<220>

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<222> (31)...(35)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 13

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu			
1	5	10	15
Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe Thr Asn Tyr			
20	25	30	
Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu Glu Trp Met			
35	40	45	
Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn Pro Ser Phe			
50	55	60	

Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr			
65	70	75	80
Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met Tyr Tyr Cys			

85

90

95

<210> 14

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<400> 14

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
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Ser	Leu	Thr	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Ser
										20	25		30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Gly	Trp	Leu
						35			40				45		
Ala	Tyr	Ile	Asp	Tyr	Gly	Ser	Ile	Phe	Ile	Tyr	Tyr	Ser	Asp	Ser	Val
							50	55			60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
					65			70			75			80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Phe	Tyr	Tyr	Cys
							85		90				95		

<210> 15

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<220>

<221> DOMAIN

<222> (31)...(35)

<223> CDRI

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<223> CDRII

<400> 15

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
 20 25 30
 Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly Pro Glu Cys Met
 35 40 45
 Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala Ile Tyr Tyr Cys
 85 90 95

<210> 16

<211> 97

<212> PRT

<213> Pan troglodytes

<220>

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<222> (31) ... (37)

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<223> CDRII

<400> 16

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
 20 25 30
 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu
 35 40 45
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
 65 70 75 80
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys

<210> 17
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<220>
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<221> DOMAIN
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<400> 17

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe Ser Thr Tyr
 20 25 30

Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Met Ile Ile Pro Ile Val Gly Thr Val Lys Tyr Ala Gln Arg Phe
 50 55 60

Gln Gly Arg Val Ser Ile Asn Ala Asp Thr Ser Thr Asn Ile Ala Tyr
 65 70 75 80
 Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

<210> 18
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<220>

<221> DOMAIN

<222> (31)...(35)

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<223> CDRII

<400> 18

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Glu	Gly	Leu	Val	Lys	Pro	Gly	Gly
1															15
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Phe
															30
Leu	Met	Phe	Trp	Val	Arg	Gln	Ala	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Val
															45
Ser	Thr	Ile	Asp	Val	Ser	Gly	Gly	Asn	Met	Trp	Tyr	Arg	Asp	Ser	Val
															50
Lys	Gly	Arg	Phe	Thr	Met	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
															60
65															80
Leu	Gln	Met	Thr	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
															85
															90
															95

<210> 19

<211> 381

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(381)

<400> 19

atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc tca

48

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Ser				
1	5	10	15	
ggc gcc aga tgt gac atc cag atg acc cag ttt cca tcc tcc ctg tct				96
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser				
20	25		30	
gca tct gta gga gac aga gtc acc atc act tgc cag tca agt cag agc				144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser				
35	40		45	
att tac aac tgc ttg agt tgg tat cag cag aaa cca ggg aag gcc cct				192
Ile Tyr Asn Cys Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro				
50	55		60	
aca ctc cta atc tat ggt gca ttc acc ttg aat agt ggg gtc cca tca				240
Thr Leu Leu Ile Tyr Gly Ala Phe Thr Leu Asn Ser Gly Val Pro Ser				
65	70	75	80	
aga ttc agt ggc agt gga tct ggc aca gat ttc act ctc acc atc agc				288
Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser				
85	90		95	
aat ctg caa cct gaa gat ttt gca aca tat tac tgt cag cgt ggt tac				336
Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Arg Gly Tyr				
100	105		110	
ggc aca cag ctc act ttc ggt gga ggg acc aag gtg gag atc aag				381
Gly Thr Gln Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys				
115	120		125	

<210> 20

<211> 384

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1) ... (384)

<400> 20

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

ctc cca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96
 Leu Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gcc agt 144
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45

cag ggc att agc aat tat tta gcc tgg tat cag cag aaa cca ggg aaa 192
 Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60

gcc cct aag ctc ctc atc tat tat gca tcc aga ttg gaa agt ggg gtc 240
 Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Arg Leu Glu Ser Gly Val
 65 70 75 80

cca tca agg ttc agc ggc agt gga tct ggg acg gat tac act ctc acc 288
 Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
 85 90 95

atc agc agc ctg cag cct gaa gat ttt gca act tat tac tgt caa cag 336
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110

tat aac agt aac ccc ttt tcg gtg gag gga cca agg tgg aga tca aac 384
 Tyr Asn Ser Asn Pro Phe Ser Val Glu Gly Pro Arg Trp Arg Ser Asn
 115 120 125

<210> 21
 <211> 384
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> CDS
 <222> (1)...(384)

<400> 21

atg tcg cca tca caa ctc att ggg ttt ctg ctg ctc tgg gtt cca gcc
 Met Ser Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala
 1 5 10 15

tcc agg ggt gaa att gtg ctg act cag tct cca gac ttt cag tct gtg
 Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val
 20 25 30

cct cca aag gag aaa gtc acc atc acc tgc cgg gcc agt cag agc att
 Pro Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
 35 40 45

ggt agt agc tta cac tgg tac cag cag aaa cca ggt cag tct cca aag
 Gly Ser Ser Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
 50 55 60

ctc ctc atc aag tat gct tcc cag tcc atc tca ggg gtc ccc tcg agg
 Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg
 65 70 75 80

tcc agt ggc agt gga tct ggg aca gat ttc acc ctc acc atc aat agc
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser
 85 90 95

ctg gaa gct gaa gat gct gca acg tat tac tgt cag caa agt agt aat
 Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Asn

100

105

110

tta cct cat acg ctc act ttc ggt gga ggg acc aag gtg gag atc aaa
 Leu Pro His Thr Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

115

120

125

384

<210> 22

<211> 372

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1) ... (372)

<400> 22

gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc tca ggt gcc
 Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Ser Gly Ala
 1 5 10 15

48

aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct
 Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 20 25 30

96

gta gga gac aga gtc acc atc act tgc cag gca agt cag agc att agc
 Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser
 35 40 45

144

aac tat ttg agt tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc
 Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 50 55 60

192

ctg atc tat gat gca tcc act ttg caa agt ggg gtc cca tca agg ttc
 Leu Ile Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe
 65 70 75 80

240

agt ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agt ctg 288
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu

85

90

95

caa cct gaa gat ttt gca aca tat tac tgt cag cgt ggt tac ggt aca 336
 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Arg Gly Tyr Gly Thr
 100 105 110

ctc act ttc ggt gga ggg acc aag gtg gag atc aaa 372
 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 115 120

<210> 23

<211> 384

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(384)

<400> 23

atg gaa gcc cca gcg cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca 48
 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
 1 5 10 15

gat acc acc gga gaa ata gtg ttg acg cag tct cca gcc acc ctg tct 96
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
 20 25 30

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45

gtt agc agg tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc 192
 Val Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro

50

55

60

agg ctc ctc atc tat ggt gca tcc aac agg gcc act ggc atc cca gcc 240
 Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
 65. 70 75 80

agg ttc agt ggc agt ggg tct agg aca gac ttc act ctc acc atc agc 288
 Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

agc gtg gag cct gaa gat ttt gca gtt tat tac tgt cag cag tat aat 336
 Ser Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn
 100 105 110

aac cag cct ctg atc gcc ttc ggc caa ggg aca cga ctg gag att aaa 384
 Asn Gln Pro Leu Ile Ala Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 115 120 125

<210> 24
 <211> 387
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> CDS
 <222> (1)...(387)

<400> 24

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15

ttc cca ggt gcc aaa tgt gac atc cag atg acc cag cag tct cct tcc acc 96
 Phe Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
 20 25 30

ctg tct gcc tcc ata gga gac aga gtc acc atc act tgt cgg gct agt 144
 Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45

cag ggc atc tat aat tat ttg aat tgg tat caq caa aaa cca ggg aga 192
 Gln Gly Ile Tyr Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg
 50 55 60

gcc cct gga ctc ctc atc ttt ggt gcc agg aat ttg gag act ggg gtc 240
 Ala Pro Gly Leu Leu Ile Phe Gly Ala Arg Asn Leu Glu Thr Gly Val
 65 70 75 80

cca tca aca ttc agc ggc agt ggt tcc ggg aca cac ttc act ctc acc 288
 Pro Ser Thr Phe Ser Gly Ser Gly Thr His Phe Thr Leu Thr
 85 90 95

atc agc agc ctg cag cct ggt gat ttt gcg act tat tac tgt cag caa 336
 Ile Ser Ser Leu Gln Pro Gly Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110

tat tat act acc ccg tat act ttt ggc cag ggg acc aag ctg gag atc 384
 Tyr Tyr Thr Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 115 120 125

aaa 387

<210> 25

<211> 387

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(387)

<400> 25

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctc tgt 48

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Cys
 1 5 10 15

ttc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tcá 96
 Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30

ctg tct gct tct gta gga gac aga gtc acc atc tct tgt cgg gcg agt 144
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser
 35 40 45

ctg gat att agc acc tgg tta gcc tgg tat cag cag aaa cca ggg aaa 192
 Leu Asp Ile Ser Thr Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60

gcc cct aag ccc ctg atc tat gct gca tcc act ttg cca agt ggg gtc 240
 Ala Pro Lys Pro Leu Ile Tyr Ala Ala Ser Thr Leu Pro Ser Gly Val
 65 70 75 80

cca tcg agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc 288
 Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95

atc agc agc ctg cag cct gaa gat tct gca act tat tac tgc cga caa 336
 Ile Ser Ser Leu Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Arg Gln
 100 105 110

 tat aat agt tat ccg ctc act ttc ggt gga ggg acc aag gtg gag atc 384
 Tyr Asn Ser Tyr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile
 115 120 125

aag 387

<210> 26

<211> 372

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1) ... (372)

<400> 26

tct	act	cag	ctc	ctg	ggg	ctc	ctg	ctc	tgg	ctc	cca	ggt	gcc	aaa	48	
Ser	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	Gly	Ala	Lys	
1			5						10					15		
tgt	gac	atc	cag	atg	acc	cag	tct	cct	tcc	acc	ctg	tct	gca	tct	gta	96
Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	
20					25								30			
gga	gac	aga	gtc	acc	atc	act	tgc	cgg	gcc	agt	cag	ggt	att	agt	agc	144
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	
35					40								45			
tgg	tta	gcc	tgg	tat	cag	cag	aaa	cca	ggg	aaa	gcc	cct	aag	ctc	ctg	192
Trp	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	
50			55							60						
atc	tat	aag	gca	tct	agt	tta	gaa	agt	ggg	gtc	cca	tca	agg	ttc	agc	240
Ile	Tyr	Lys	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	
65			70							75			80			
ggc	agt	gga	tct	ggg	aca	gaa	ttc	act	ctc	acc	atc	agc	agc	ctg	cag	288
Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	
85					90								95			
cct	gat	gat	ttt	gca	act	tat	tac	tgc	caa	cag	tat	agt	agt	tac	cct	336
Pro	Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Ser	Tyr	Pro	
100					105								110			
cga	acg	ttc	ggc	caa	ggg	acc	aag	ctg	gaa	atc	aaa					372
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
115					120											

<210> 27
 <211> 387
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> CDS
 <222> (1) . . . (387)

<400> 27

atg	gac	atg	agg	gtc	ccc	gct	cag	ctc	ctg	ggg	ctc	ctg	ctg	ctc	tgg	48
Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	
1		5							10					15		
ctc	tca	ggt	acc	aga	tgt	gac	atc	cag	atg	acc	cag	tct	cca	tcc	tcc	96
Leu	Ser	Gly	Thr	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	
20								25					30			
ctg	tct	gca	tct	gta	gga	gac	aga	gtc	acc	atc	act	tgc	cgg	gca	agt	144
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	
35								40					45			
cag	agc	att	agc	aac	tat	ttg	agt	tgg	tat	cag	cag	aaa	cca	ggg	aaa	192
Gln	Ser	Ile	Ser	Asn	Tyr	Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	
50								55					60			
gcc	cct	aag	ctc	ctg	atc	tat	tat	gca	tcc	act	ttg	caa	agt	ggg	gtc	240
Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	
65								70					75			
cca	tca	agg	ttc	agt	ggc	agt	gga	tct	ggg	aca	gat	ttc	act	ctc	acc	288
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
85									90					95		
atc	agc	agt	ctg	caa	cct	gaa	gat	ttt	gca	act	tat	tac	tgt	cag	cat	336

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His

100

105

110

ggt tac ggt aca cat ccc act ttc ggt gga ggg acc aag gtg gag atc

384

Gly Tyr Gly Thr His Pro Thr Phe Gly Gly Thr Lys Val Glu Ile

115

120

125

aaa

387

<210> 28

<211> 88

<212> PRT

<213> Pan troglodytes

<220>

<221> DOMAIN

<222> (24)...(34)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 28

Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Ile Tyr Asn Cys

20

25

30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile

35

40

45

Tyr Gly Ala Phe Thr Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys

85

<210> 29
 <211> 88
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> DOMAIN
 <222> (24) ... (34)
 <223> CDRI

<221> DOMAIN
 <222> (50) ... (66)
 <223> CDRII

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys
 85

<210> 30
 <211> 88
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> DOMAIN
 <222> (24) ... (34)
 <223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 30

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Pro Pro Lys

1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser Ser

20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala

65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys

85

<210> 31

<211> 88

<212> PRT

<213> Pan troglodytes

<220>

<221> DOMAIN

<222> (24)...(34)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Asn Tyr

20

25

30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys

85

<210> 32

<211> 88

<212> PRT

<213> Pan troglodytes

<220>

<221> DOMAIN

<222> (24)...(34)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 32

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr

20

25

30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35

40

45

Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly

50

55

60

Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Glu Pro

65

70

75

80

Glu Asp Phe Ala Val Tyr Tyr Cys

85

<210> 33
 <211> 88
 <212> PRT
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<220>
 <221> DOMAIN
 <222> (24) ... (34)
 <223> CDRI

<221> DOMAIN
 <222> (50) ... (66)
 <223> CDRII

<400> 33

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Tyr Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Gly Leu Leu Ile
 35 40 45
 Phe Gly Ala Arg Asn Leu Glu Thr Gly Val Pro Ser Thr Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Gly Asp Phe Ala Thr Tyr Tyr Cys

85

<210> 34
 <211> 88
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> DOMAIN
 <222> (24) ... (34)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 34

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1															15

Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Leu	Asp	Ile	Ser	Thr	Trp
															30
20															

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Leu	Ile
35															45

Tyr	Ala	Ala	Ser	Thr	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
50															60

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65															80

Glu	Asp	Ser	Ala	Thr	Tyr	Tyr	Cys								
				85											

<210> 35

<211> 88

<212> PRT

<213> Pan troglodytes

<220>

<221> DOMAIN

<222> (24)...(34)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 35

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1															15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys
 85

<210> 36

<211> 88

<212> PRT

<213> Pan troglodytes

<220>

<221> DOMAIN

<222> (24)...(34)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys

<210> 37

<211> 408

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(408)

<400> 37

atg gag ttt gga ctg agc tgg gtt ttc ctt gtc gct att ttc aaa ggt
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Phe Lys Gly

1 5 10 15

gtc cag tgt gaa gtg cag ttg gtg gag tct ggg gga ggc ttg gta cag
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln

20 25 30

ccg ggg ggg tcc ctg aga ctc gcc tgt gta ggc tct gga ttc gcc ttc
 Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe

35 40 45

aga aac acc agg atg cac tgg att cga cag act cca gga aag agg ctg
 Arg Asn Thr Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu

50 55 60

gag tgg gtg gcc gac ata aag ttt gat gga agt gat ttt tac tat gta
 Glu Trp Val Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val

65 70 75 80

gac tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn

85 90 95

tcc ctc tat ctg gaa atg aac agc ctg aga cct gat gac aca gcc gtc

48

96

144

192

240

288

336

Ser Leu Tyr Leu Glu Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Val
 100 105 110

384
 tat ttc tgt gtg aga gaa tac aga gat gga ctg gat gtc tgg ggc cgg
 Tyr Phe Cys Val Arg Glu Tyr Arg Asp Gly Leu Asp Val Trp Gly Arg
 115 120 125

408
 gga gtt ctg gtc acc gtc tcc tca
 Gly Val Leu Val Thr Val Ser Ser
 130 135

<210> 38

<211> 381

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(381)

<400> 38

48
 gtg aca gct ccc aga tgg gtc ctg tcc cag gtg caa ttg cag gag tcg
 Val Thr Ala Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ser
 1 5 10 15

96
 ggc cca gga ctg gtg aag cct tcg gag acc ctg tcc ctc act tgt act
 Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
 20 25 30

144
 gtc tct ggt gac tcc atc acc act gtc ttc tgg agc tgg ctc cgc cag
 Val Ser Gly Asp Ser Ile Thr Thr Val Phe Trp Ser Trp Leu Arg Gln
 35 40 45

192
 tcg cca ggg att ggg ctg gag tgg att ggg aat ttt gct ggt agt act
 Ser Pro Gly Ile Gly Leu Glu Trp Ile Gly Asn Phe Ala Gly Ser Thr
 50 55 60

ccg gaa acg aac tac aat ccc tcc ctc aag aat cga gcc acc att tca	240
Pro Glu Thr Asn Tyr Asn Pro Ser Leu Lys Asn Arg Ala Thr Ile Ser	
65 70 75 80	
aaa gac acg ccc acg aat caa ttt ttc ctg agg ctg acg tct gtg acc	288
Lys Asp Thr Pro Thr Asn Gln Phe Phe Leu Arg Leu Thr Ser Val Thr	
85 90 95	
gcc gcg gac acg gcc gtc tac ttc tgt gcg aga gga ggg gga gcc ggc	336
Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg Gly Gly Ala Gly	
100 105 110	
aac cca ctc act tgg ggc cag gga gtc cag gtc acc gtc tcc tca	381
Asn Pro Leu Thr Trp Gly Gln Gly Val Gln Val Thr Val Ser Ser	
115 120 125	
<210> 39	
<211> 417	
<212> DNA	
<213> Macaca cynomolgus	
<220>	
<221> CDS	
<222> (1)...(417)	
<400> 39	
atg ggg tca act gcc atc ctc gcc ctc ctc ctg gct gtt ctc caa gga	48
Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly	
1 5 10 15	
gtc tgt gcc gag gtg cat ctg gtg cag tct gga gca cag gtg aaa agg	96
Val Cys Ala Glu Val His Leu Val Gln Ser Gly Ala Gln Val Lys Arg	
20 25 30	
ccc ggg gaa tct ctg agg atc tcc tgt aag act tct gga tac acc ttt	144

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
 35 40 45

acc gac agc tgg atc agc tgg gtg cgc cag atg ccc ggg aaa ggc ctg 192
 Thr Asp Ser Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 50 55 60

gag tgg atg gga aac atc tat cct ggt gat tct gat tcc aga tac aac 240
 Glu Trp Met Gly Asn Ile Tyr Pro Gly Asp Ser Asp Ser Arg Tyr Asn
 65 70 75 80

ccg tcc ttc caa ggc cgc gtc act atc tca gtc gac aag tcc atc agt 288
 Pro Ser Phe Gln Gly Arg Val Thr Ile Ser Val Asp Lys Ser Ile Ser
 85 90 95

acc acc tac ctg cag tgg agc agc ctg aag gcc tcg gac act gcc aca 336
 Thr Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Thr
 100 105 110

tat tac tgt gcg aag ata gat agc aac tac tac agc cgg ttc gaa gtc 384
 Tyr Tyr Cys Ala Lys Ile Asp Ser Asn Tyr Tyr Ser Arg Phe Glu Val
 115 120 125

tgg ggc ccc gga gtc atg gtc acc gtc tcc tca 417
 Trp Gly Pro Gly Val Met Val Thr Val Ser Ser
 130 135

<210> 40

<211> 423

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1) ... (423)

<400> 40

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct cct aga tgg	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
gtc ctg tcc cag gtg cag ttg cag gag tcg ggc cca gga gtg gtg aag	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys	
20 25 30	
cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc ttc	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe	
35 40 45	
agt act tac tac tgg aat tgg atc cgc cag ccc cca ggg aag gga ctg	192
Ser Thr Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu	
50 55 60	
gag tgg att gga tat atc ggt ggt ggt ggt cgc ccc aac tac aat	240
Glu Trp Ile Gly Tyr Ile Gly Gly Gly Arg Pro Asn Tyr Asn	
65 70 75 80	
tcc tcc ctc aag agt cgc atc acc ctg tca cta gac gcg tcc aag aac	288
Ser Ser Leu Lys Ser Arg Ile Thr Leu Ser Leu Asp Ala Ser Lys Asn	
85 90 95	
cag ttc tcc ctg aac ctg agc tct gtg acc gcc gcg gac acg gcc gtg	336
Gln Phe Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
— tac tac tgt gcc aga gat cgg ggc tac ggt gcc agc aat gat gct ttt	384
Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Gly Ala Ser Asn Asp Ala Phe	
115 120 125	
gat ttc tgg ggc caa ggg ctc agg gtc acc gtc tct tca	423
Asp Phe Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser	
130 135 140	

<210> 41
 <211> 411
 <212> DNA
 <213> *Macaca cynomolgus*

<220>
 <221> CDS
 <222> (1) ... (411)

<400> 41

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca act cct aaa tgg 48
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Thr Pro Lys Trp
 1 5 10 15

gtc ctg tcc cag gtg cag ttg cat gag tcg ggc cct gga ctg ctg aag 96
 Val Leu Ser Gln Val Gln Leu His Glu Ser Gly Pro Gly Leu Leu Lys
 20 25 30

cct tcg gag acc ctg tcc ctc acc tgc aat gtc tcc ggt gac tcc ccc 144
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Asn Val Ser Gly Asp Ser Pro
 35 40 45

act aag tcc acg tgg aac tgg gtc cgc cag tcc cca ggg aag cca ctg 192
 Thr Lys Ser Thr Trp Asn Trp Val Arg Gln Ser Pro Gly Lys Pro Leu
 50 55 60

gaa tgg att ggt cat gtc ggt tct ggt gga ggt ggc ccc gtt tac aac 240
 Glu Trp Ile Gly His Val Gly Ser Gly Gly Gly Pro Val Tyr Asn
 65 70 75 80

gtc ttc ttg acg ggt cgc gtc tcc atg tct cta gac gct tca aag aag 288
 Val Phe Leu Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys
 85 90 95

ctt ctc tcc ctg gcc tta gca tct gtg acc gcc gcc gac tcg gcc gtc 336
 Leu Leu Ser Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val

100

105

110

tat tac tgt gtc aga tcg acg gca tta ttt tcg ttg gat gtc tgg ggc
 Tyr Tyr Cys Val Arg Ser Thr Ala Leu Phe Ser Leu Asp Val Trp Gly

384

115

120

125

cgg gga ctt ctg gtc acc gtc tcc tca
 Arg Gly Leu Leu Val Thr Val Ser Ser

411

130

135

<210> 42

<211> 442

<212> DNA

<213> Macaca cynomolgus.

<220>

<221> CDS

<222> (1)...(441)

<400> 42

atg gag ttg gga ctg agc tgg gtt ttc ctt ctt gtt gct att tta aaa
 Met Glu Leu Gly Leu Ser Trp Val Phe Leu Leu Val Ala Ile Leu Lys

48

1

5

10

15

ggt gtc cag tgt gac aag cag ctg gtg cag tcg ggg gga ggc ttg gtc
 Gly Val Gln Cys Asp Lys Gln Leu Val Gln Ser Gly Gly Gly Leu Val

96

20

25

30

cag cct ggc ggg tct ctg aga ctc gcc tgt gta gcc tcc gga ttc ccc
 Gln Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro

144

35

40

45

ttc agt gac tat tac atg agt tgg gtc cgc cag gct cca ggg aag ggg
 Phe Ser Asp Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly

192

50

55

60

ttg gag tgg ctt gga tta att aaa acc aat cct gat ggt gga acg aca 240
 Leu Glu Trp Leu Gly Leu Ile Lys Thr Asn Pro Asp Gly Gly Thr Thr
 65 70 75 80

gat tac gcc gcg tct gtg aaa ggc aga ttt atc atc tca cga gat gat 238
 Asp Tyr Ala Ala Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asp
 85 90 95

tca aag aac tca ctg ttc ctt caa atg aac agc ctg aaa acc gag gac 336
 Ser Lys Asn Ser Leu Phe Leu Gln Met Asn Ser Leu Lys Thr Glu Asp
 100 105 110

acg gcc gtg tat tac tgc acc aca gaa gtg ttg gtg gtg tct gct att 384
 Thr Ala Val Tyr Tyr Cys Thr Thr Glu Val Leu Val Val Ser Ala Ile
 115 120 125

caa ctc att gga tgt ctg ggg ccc ggg gag ttg tgg tca ccc gtc tct 432
 Gln Leu Ile Gly Cys Leu Gly Pro Gly Glu Leu Trp Ser Pro Val Ser
 130 135 140

ttc cgc ttc a 442
 Phe Arg Phe
 145

<210> 43

<211> 407

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(405)

<400> 43

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1	5	10	15	
				96
gtc ctg tcc cag gtg cag ttg gag gag tcg ggc cca gga ctg gtg aag Val Leu Ser Gln Val Gln Leu Glu Glu Ser Gly Pro Gly Leu Val Lys				
20	25	30		
				144
ccc tcg gag acc ctg tcc ctc acc tgc gct gtg tct ggt ggc ctc att Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Leu Ile				
35	40	45		
				192
act gga aac tac tgg aac tgg ctc cgg cag tca gaa ggg aag gga ctg Thr Gly Asn Tyr Trp Asn Trp Leu Arg Gln Ser Glu Gly Lys Gly Leu				
50	55	60		
				240
gag tgg att ggc cat att ggt ggt agt agt ggg aac acc ggc tac aac Glu Trp Ile Gly His Ile Gly Gly Ser Ser Gly Asn Thr Gly Tyr Asn				
65	70	75	80	
				288
tcc gct ttc gag agt cgc gtc acc ttg tca aga gac acg gcc aag aat Ser Ala Phe Glu Ser Arg Val Thr Leu Ser Arg Asp Thr Ala Lys Asn				
85	90	95		
				336
cggttc tcc ctg aaa ctg acc tct gtg acc gcc gca gat tcg gcc gtc Arg Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Ser Ala Val				
100	105	110		
				384
tat tac tgt gcg aga tcg ggt ttt acc ggc acc gac ttc ttt tac tat Tyr Tyr Cys Ala Arg Ser Gly Phe Thr Gly Thr Asp Phe Phe Tyr Tyr				
115	120	125		
				407
tgg ggc ccg ggg aag tct tgg tc Trp Gly Pro Gly Lys Ser Trp				
130	135			

<210> 44

<211> 420

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(420)

<400> 44

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg	48		
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp			
1	5	10	15
gtc ctg tcc cag gtt caa cta cag gag tcg ggc cca gga ctg atg aag	96		
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Met Lys			
20	25	30	
cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tcc atc	144		
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile			
35	40	45	
agc ggt ggt ttt ggc tgg ggc tgg atc cgt cag tcc ccg ggg aag ggg	192		
Ser Gly Gly Phe Gly Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly			
50	55	60	
ctg gaa tgg att gga agt ttc tat act act act gga aat acc ttc tcc	240		
Leu Glu Trp Ile Gly Ser Phe Tyr Thr Thr Gly Asn Thr Phe Ser			
65	70	75	80
aac ccc tcc ctc aag agt cga gtc acc att tca gcg gac acg tcc aag	288		
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys			
85	90	95	
aac cag ttc tcc ctg aga ctg acc tct gtg acc gcc gcg gac acg gcc	336		
Asn Gln Phe Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala			
100	105	110	
gtt tat tac tgt gcg aga gat ctc tat agc agc ggc tat aaa ttt tac	384		

Val Tyr Tyr Cys Ala Arg Asp Leu Tyr Ser Ser Gly Tyr Lys Phe Tyr
 115 120 125

tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 420
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
 130 135 140

<210> 45

<211> 98

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (31) ... (35)

<223> CDRI

<221> DOMAIN

<222> (50) ... (66)

<223> CDRII

<400> 45

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe Arg Asn Thr
 20 25 30

Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Val
 35 40 45

Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Val Arg

<210> 46
 <211> 98
 <212> PRT
 <213> *Macaca cynomolgus*

<220>
 <221> DOMAIN
 <222> (31)...(35)
 <223> CDRI

<221> DOMAIN
 <222> (50)...(66)
 <223> CDRII

<400> 46

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Thr Thr Val
 20 25 30
 Phe Trp Ser Trp Leu Arg Gln Ser Pro Gly Ile Gly Leu Glu Trp Ile
 35 40 45
 Gly Asn Phe Ala Gly Ser Thr Pro Glu Thr Asn Tyr Asn Pro Ser Leu
 50 55 60
 Lys Asn Arg Ala Thr Ile Ser Lys Asp Thr Pro Thr Asn Gln Phe Phe
 65 70 75 80
 Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg

<210> 47
 <211> 98
 <212> PRT
 <213> *Macaca cynomolgus*

<220>

<221> DOMAIN

<222> (31)...(35)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 47

Glu	Val	His	Leu	Val	Gln	Ser	Gly	Ala	Gln	Val	Lys	Arg	Pro	Gly	Glu
1															
Ser	Leu	Arg	Ile	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Ser
	20						25					30			
Trp	Ile	Ser	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
	35					40						45			
Gly	Asn	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Ser	Arg	Tyr	Asn	Pro	Ser	Phe
	50											60			
Gln	Gly	Arg	Val	Thr	Ile	Ser	Val	Asp	Lys	Ser	Ile	Ser	Thr	Thr	Tyr
	65						70					75		80	
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys
												85	90	95	
Ala	Lys														

<210> 48

<211> 98

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (31)...(35)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 48

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Val	Val	Lys	Pro	Ser	Glu
1															15
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Phe	Ser	Thr	Tyr
	20						25							30	
Tyr	Trp	Asn	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35					40							45	
Gly	Tyr	Ile	Gly	Gly	Gly	Gly	Arg	Pro	Asn	Tyr	Asn	Ser	Ser	Leu	
		50					55							60	
Lys	Ser	Arg	Ile	Thr	Leu	Ser	Leu	Asp	Ala	Ser	Lys	Asn	Gln	Phe	Ser
		65					70							80	
Leu	Asn	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85						90			95	
Ala	Arg														

<210> 49

<211> 98

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (31)...(35)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 49

Gln	Val	Gln	Leu	His	Glu	Ser	Gly	Pro	Gly	Leu	Leu	Lys	Pro	Ser	Glu
1															15
Thr	Leu	Ser	Leu	Thr	Cys	Asn	Val	Ser	Gly	Asp	Ser	Pro	Thr	Lys	Ser
	20						25						30		
Thr	Trp	Asn	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Pro	Leu	Glu	Trp	Ile

35	40	45
Gly His Val Gly Ser Gly Gly Gly Pro Val Tyr Asn Val Phe Leu		
50	55	60
Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys Leu Leu Ser		
65	70	75
Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys		
85	90	95
Val Arg		

<210> 50
 <211> 100
 <212> PRT
 <213> Macaca cynomolgus

<220>
 <221> DOMAIN
 <222> (31)...(35)
 <223> CDRI

<221> DOMAIN
 <222> (50)...(68)
 <223> CDRII

<400> 50

Asp Lys Gln Leu Val Gln Ser Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10
Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro Phe Ser Asp Tyr		
20	25	30
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu		
35	40	45
Gly Leu Ile Lys Thr Asn Pro Asp Gly Gly Thr Thr Asp Tyr Ala Ala		
50	55	60
Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asp Ser Lys Asn Ser		
65	70	75
Leu Phe Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr		
85	90	95

Tyr Cys Thr Thr

100

<210> 51

<211> 98

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (31)...(35)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 51

Gln Val Gln Leu Glu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Leu Ile Thr Gly Asn

20 25 30

Tyr Trp Asn Trp Leu Arg Gln Ser Glu Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly His Ile Gly Gly Ser Ser Gly Asn Thr Gly Tyr Asn Ser Ala Phe

50 55 60

Glu Ser Arg Val Thr Leu Ser Arg Asp Thr Ala Lys Asn Arg Phe Ser

65 70 75 80

Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys

85 90 95

Ala Arg

<210> 52

<211> 99

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (31)...(36)

<223> CDRI

<221> DOMAIN

<222> (51)...(67)

<223> CDRII

<400> 52

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Met	Lys	Pro	Ser	Glu
1															
1															15

Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Ile	Ser	Gly	Gly
															30
20															

Phe	Gly	Trp	Gly	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp
															45
35															

Ile	Gly	Ser	Phe	Tyr	Thr	Thr	Thr	Gly	Asn	Thr	Phe	Ser	Asn	Pro	Ser
															50
50															
															55

Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Gln	Phe
															65
65															
															80

Ser	Leu	Arg	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
															85
85															
															90

Cys	Ala	Arg													

<210> 53

<211> 390

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(390)

<400> 53

atg gac ata agg gtc ccc gtg cag ctc ctg ggg ctc ctg ttg ctc tgg

48

Met Asp Ile Arg Val Pro Val Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15

ctc cga ggt gcc aga tgt gac atc cag atg acc cag cag tct cca tcc tcc 96
 Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30

ctg tct aca tct gta gga gac act gtc acc atc act tgc cgg gcg agt 144
 Leu Ser Thr Ser Val Gly Asp Thr Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45

caa ggc att gac acg gag tta gcc tgg tat cag cag aaa cca ggt aaa 192
 Gln Gly Ile Asp Thr Glu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60

gcc ccc aca ctc ctg atc tct gat gcc tcc agg ttg cag acg ggg gtc 240
 Ala Pro Thr Leu Leu Ile Ser Asp Ala Ser Arg Leu Gln Thr Gly Val
 65 70 75 80

tca tct cgg ttc agc ggc agt gga tct gga aca gat ttc act ctc acc 288
 Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95

atc aac agc ctg cag cct gaa gat att gcg act tat tac tgtcaa cag 336
 Ile Asn Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110

gat aat agt ttt cca ctc act ttc ggc gga ggg acc aag gtg gag atc 384
 Asp Asn Ser Phe Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile
 115 120 125

aaa cga 390
 Lys Arg
 130

<211> 384

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1) ... (384)

<400> 54

gtc ttc att tcc ctg ttg ctc tgg atc tct ggt gcc tgt ggg gac att
 Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Cys Gly Asp Ile
 1 5 10 15

48

gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg gga gag agg
 Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
 20 25 30

96

gtc acc atc aat tgt aag tcc agc cag agt ctt tta tac agc tcc aac
 Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn
 35 40 45

144

aat aag aac tac tta gcc tgg tac cag caa aaa cca gga cag gct cct
 Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 50 55 60

192

caa cta ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc cct aat
 Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asn
 65 70 75 80

240

cga ttt agt ggc agc ggc tct ggg aca gat ttc act ctc acc atc agt
 Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

288

ggc ctg cag gct gaa gat gtg gca gtg tat tac tgt caa cag tat tat
 Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
 100 105 110

336

gat atg ccc gac agt ttt ggc cag ggg acc aaa gtc gac atc aaa cga 384
 Asp Met Pro Asp Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
 115 120 125

<210> 55
 <211> 399
 <212> DNA
 <213> Macaca cynomolgus

<220>
 <221> CDS
 <222> (1)...(399)

<400> 55

atg agg ctc cct gct cag ctc ctg ggg ctg cta ttg ctc tgc gtc ccc 48
 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Cys Val Pro
 1 5 10 15

gga tcc agt ggg gat gtt gtg atg act cag tct cca ctc tcc ctg ccc 96
 Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 20 25 30

gtc atc cct gga cag cca gcc tcc atc tcc tgc agg tct agt caa agc 144
 Val Ile Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 35 40 45

ctt gta cat agt gac ggg aaa acc tac ttg aat tgg tta caa cag aag 192
 Leu Val His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys
 50 55 60

cca ggc caa cct cca aga ctc ctg att tat cag gtt tct aac cgg cac 240
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Gln Val Ser Asn Arg His
 65 70 75 80

tct ggg gtc cca gac aga ttc agc ggc agt ggg gca ggg aca gac ttc 288
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe

85

90

95

aca ctg aaa atc agc aga gtg gag act gag gat gtt ggg gtt tat tcc 336
 Thr Leu Lys Ile Ser Arg Val Glu Thr Glu Asp Val Gly Val Tyr Ser

100

105

110

tgc gtg caa ggt aca cac tgg ccg tgg acg ttc ggc caa ggg acc aag 384
 Cys Val Gln Gly Thr His Trp Pro Trp Thr Phe Gly Gln Gly Thr Lys
 115 120 125

gtg gac atc aaa cga 399
 Val Asp Ile Lys Arg
 130

<210> 56

<211> 384

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(384)

<400> 56

atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca 48
 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro

1

5

10

15

ggc gcc ata tgt gac att cag atg tcc cag tct cca tcc tcc ctg tct 96
 Gly Ala Ile Cys Asp Ile Gln Met Ser Gln Ser Pro Ser Ser Leu Ser

20

25

30

gct tct gtg gga gac aga gtc acc atc acc tgc cgg gca agt cag ggc 144
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly

35

40

45

ata act aat tat tta aac tgg tat cag cag aaa ccg ggg aaa gcc cct	50	55	60	192
Ile Thr Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro				
aac ctc ctg atc tat tat gca act cgt ttg gcg agc ggg gtc cca tca	65	70	75	240
Asn Leu Leu Ile Tyr Tyr Ala Thr Arg Leu Ala Ser Gly Val Pro Ser				
agg ttc agc ggc agt gga tct ggg tcg gag tac agt ctc gcc atc agc	85	90	95	288
Arg Phe Ser Gly Ser Gly Ser Glu Tyr Ser Leu Ala Ile Ser				
agc ctg cag cct gaa gat ttt gca acc tat ttc tgt caa cag ggt tat	100	105	110	336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Tyr				
agg gcc ccc tac act ttt ggc cag ggg acc aca gtg gag atc aaa cga	115	120	125	384
Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg				
<210> 57				
<211> 390				
<212> DNA				
<213> Macaca cynomolgus				
<220>				
<221> CDS				
<222> (1)...(390)				
<400> 57				
atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg	1	5	10	48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp				
ctc cta ggt gcc aga tgt gac atc cag atg acc cag cag tct cct tct tcc				96
Leu Leu Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser				

20

25

30

ttg tct gca tct gta gga gac aga gtc acc atc act tgc caa gcc agt 144
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser

35 40

45

cag ggt att agc aac tgg tta gcc tgg tat cag cag aaa ccg ggg aaa 192
 Gln Gly Ile Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60

gcc cct aag ctc ctg atc tat gct gca tcc act ttc caa agt ggg gtc 240
 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val
 65 70 75 80

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
 85 90 95

atc agc agc ctg cag cct gaa gat ttt gca act tac tac tgt caa cag 336
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110

tat aat act tac cct ctc act ttc ggc gga ggg acc aag gtg gag atc. 384
 Tyr Asn Thr Tyr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile
 115 120 125

aaa cga 390
 Lys Arg
 130

<210> 58

<211> 390

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1) ... (390)

<400> 58

atg gac ttg agg gcc ccc gct cat ctc cta ggg ctc ctg ctg ctc tgg
 Met Asp Leu Arg Ala Pro Ala His Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15

48

ctc cca ggt gcc aga ggt gac atc cag atg acc cag tct cca ccc tcc
 Leu Pro Gly Ala Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Pro Ser
 20 25 30

96

ctg tct gcg tct gtt ggg gac act gtc agt ctt act tgt cgg gca agt
 Leu Ser Ala Ser Val Gly Asp Thr Val Ser Leu Thr Cys Arg Ala Ser
 35 40 45

144

cag cct att ggc agt aat tta aat tgg ttc cag caa aaa cct ggg agc
 Gln Pro Ile Gly Ser Asn Leu Asn Trp Phe Gln Gln Lys Pro Gly Ser
 50 55 60

192

ccc ccc aga ctc ctg atc tac ctt gcg acc gcc ttg caa cgt ggg atc
 Pro Pro Arg Leu Leu Ile Tyr Leu Ala Thr Ala Leu Gln Arg Gly Ile
 65 70 75 80

240

ccg tca agg ttt agc gcc act gga tct caa acc aat ttc act ctc acg
 Pro Ser Arg Phe Ser Ala Thr Gly Ser Gln Thr Asn Phe Thr Leu Thr
 85 90 95

288

atc acc ggc ctg cag cct gag gat ttc gca act tac ctc tgt ctg caa
 Ile Thr Gly Leu Gln Pro Glu Asp Phe Ala Thr Tyr Leu Cys Leu Gln
 100 105 110

336

cat act tct tac cca ttc act ttt ggc ccc ggg aca aag gtg gat atc
 His Thr Ser Tyr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
 115 120 125

384

aag cga

390

Lys Arg

130

<210> 59

<211> 88

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (24) ... (34)

<223> CDRI

<221> DOMAIN

<222> (50) ... (56)

<223> CDRII

<400> 59

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Thr Ser Val Gly

1 5 10 15

Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asp Thr Glu

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile

35 40 45

Ser Asp Ala Ser Arg Leu Gln Thr Gly Val Ser Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro

65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys

85

<210> 60

<211> 94

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (24)...(40)

<223> CDRI

<221> DOMAIN

<222> (56)...(62)

<223> CDRII

<400> 60

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Glu Arg Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Ala Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
 85 90

<210> 61

<211> 93

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (24)...(39)

<223> CDRI

<221> DOMAIN

<222> (54)...(61)

<223> CDRII

<400> 61

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ile Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Gln Val Ser Asn Arg His Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Thr Glu Asp Val Gly Val Tyr Ser Cys
 85 90

<210> 62

<211> 88

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (24) ... (34)

<223> CDRI

<221> DOMAIN

<222> (50) ... (56)

<223> CDRII

<400> 62

Asp Ile Gln Met Ser Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
 35 40 45
 Tyr Tyr Ala Thr Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Ser Glu Tyr Ser Leu Ala Ile Ser Ser Leu Gln Pro
 65. 70 75 80
 Glu Asp Phe Ala Thr Tyr Phe Cys
 85

<210> 63
 <211> 88
 <212> PRT
 <213> Macaca cynomolgus

<220>
 <221> DOMAIN
 <222> (24)...(34)
 <223> CDRI

<221> DOMAIN
 <222> (50)...(56)
 <223> CDRII

<400> 63

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Gly Ile Ser Asn Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys
 85

<210> 64
 <211> 88
 <212> PRT
 <213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (24) ... (34)

<223> CDRI

<221> DOMAIN

<222> (50) ... (56)

<223> CDRII

<400> 64

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Pro	Ser	Leu	Ser	Ala	Ser	Val	Gly
1															
				5						10					15

Asp	Thr	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Pro	Ile	Gly	Ser	Asn
				20					25						30

Leu	Asn	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Pro	Pro	Arg	Leu	Leu	Ile
				35				40							45

Tyr	Leu	Ala	Thr	Ala	Leu	Gln	Arg	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Ala
			50				55								60

Thr	Gly	Ser	Gln	Thr	Asn	Phe	Thr	Leu	Thr	Ile	Thr	Gly	Leu	Gln	Pro
			65			70			75						80

Glu	Asp	Phe	Ala	Thr	Tyr	Leu	Cys								
				85											

<210> 65

<211> 360

<212> DNA

<213> Rat

<220>

<221> CDS

<222> (1) ... (360)

<400> 65

gac	acg	gtg	ctg	acc	cag	tct	cct	gct	ttg	gct	gtg	cct	cca	gga	gag
Asp	Thr	Val	Leu	Thr	Gln	Ser	Pro	Ala	Leu	Ala	Val	Pro	Pro	Gly	Glu
1									5						10
															15

48

agg gtt acc gtc tcc tgt agg gcc agt gaa agt gtc agt aca ttt ttg	96		
Arg Val Thr Val Ser Cys Arg Ala Ser Glu Ser Val Ser Thr Phe Leu			
20	25	30	
cac tgg tat caa cag aaa cca gga cat caa ccc aaa ctc ctc atc tat	144		
His Trp Tyr Gln Gln Lys Pro Gly His Gln Pro Lys Leu Leu Ile Tyr			
35	40	45	
cta gcc tca aaa cta gaa tct ggg gtc cct gcc agg ttc agt ggc ggt	192		
Leu Ala Ser Lys Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Gly			
50	55	60	
ggg tct ggg aca gac ttc acc ctc acc att gat cct gtg gag gct gat	240		
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp			
65	70	75	80
gac act gct acc tat tac tgt cag cag acc tgg aat gat cct cgg acg	288		
Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Asn Asp Pro Arg Thr			
85	90	95	
ttc ggt gga ggc acc aag ctg gaa ttg aaa cgg gct gat gct gca cca	336		
Phe Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro			
100	105	110	
act gta tct atc ttc cca cca tcc	360		
Thr Val Ser Ile Phe Pro Pro Ser			
115	120		

<210> 66

<211> 360

<212> DNA

<213> Rat

<220>

<221> CDS

<222> (1)...(360)

<400> 66

gag	gtc	cag	ctg	cag	cag	tct	gga	cct	gag	gtt	ggg	agg	cct	ggg	tcc	48
Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Val	Gly	Arg	Pro	Gly	Ser	
1			5						10				15			
tca gtc aag att tct tgc aag gct tct ggc tac acc ttt aca gat tac																96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr																
20							25					30				
gtt ttg aat tgg gtg aag cag agt cct gga cag gga ctg gaa tgg ata																144
Val	Leu	Asn	Trp	Val	Lys	Gln	Ser	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	
35							40					45				
gga tgg att gat cct gac tat ggt act act gat tat gct gag aag ttc																192
Gly	Trp	Ile	Asp	Pro	Asp	Tyr	Gly	Thr	Thr	Asp	Tyr	Ala	Glu	Lys	Phe	
50							55					60				
aaa aag aag gcc aca ctg act gca gat aca tcc tcc agc aca gcc tac																240
Lys	Lys	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr	
65							70					75			80	
atc cag ctt agc agc ctg aca tct gag gac aca gcc acc tat ttt tgt																288
Ile	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
85							90					95				
gct aga tct agg aat tac gga gga tat att aat tac tgg ggc caa gga																336
Ala	Arg	Ser	Arg	Asn	Tyr	Gly	Gly	Tyr	Ile	Asn	Tyr	Trp	Gly	Gln	Gly	
100							105					110				
gtc atg gtc aca gtc tcc tca gct																360
Val	Met	Val	Thr	Val	Ser	Ser	Ala									
115							120									

<210> 67

<211> 109

<212> PRT

<213> Pan troglodytes

<400> 67

Ala Val His Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Asn Ile Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Phe Asp Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Arg Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Cys Gly Trp Gly Thr His Pro
 85 90 95
 Tyr Asn Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 68

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> rat/chimpanzee sequence

<400> 68

Asp Thr Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Ser Thr Phe
 20 25 30
 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Lys Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Arg Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Asn Asp Pro Arg
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 69
 <211> 128
 <212> PRT
 <213> Pan troglodytes

<400> 69

Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Phe
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Ser Leu Val Ser Trp Asp Ser Tyr Asn Ile Tyr His Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Asp Leu Arg Pro Glu Asp Thr Ala Ile Tyr Phe Cys
 85 90 95
 Ala Lys Ala Asp Thr Gly Gly Asp Phe Asp Tyr Val Ser Asp Ser Trp
 100 105 110

Arg Cys Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125

<210> 70
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> rat/chimpanzee sequence

<400> 70

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Val Leu Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Trp Ile Asp Pro Asp Tyr Gly Thr Thr Asp Tyr Ala Glu Lys Phe
 50 55 60
 Lys Lys Lys Ala Thr Leu Ser Ala Asp Thr Ser Arg Asn Ser Ala Tyr
 65 70 75 80
 Leu Gln Met Asn Asp Leu Arg Pro Glu Asp Thr Ala Ile Tyr Phe Cys
 85 90 95
 Ala Arg Ser Arg Asn Tyr Gly Gly Tyr Ile Asn Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser
 115

<210> 71

<211> 354

<212> DNA

<213> Murine

<220>

<221> CDS

<222> (1)...(354)

<400> 71

caa gtt cag ctt caa cag tct gga gct gag ctg atg aag cct ggg gcc 48
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
 1 5 10 15

tca gtg aag ata tcc tgc aag gct act ggc tac aca ttc agt agc tac 96
 Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr
 20 25 30

tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att 144
 Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
 35 40 45

gga gag att tta cct aga agt ggt aat act aac tac aat gag aag ttc 192
 Gly Glu Ile Leu Pro Arg Ser Gly Asn Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

aag ggc aag gcc aca ttc act gca gaa aca tcc tcc aac aca gcc tac 240
 Lys Gly Lys Ala Thr Phe Thr Ala Glu Thr Ser Ser Asn Thr Ala Tyr
 65 70 75 80

atg caa ctc agc agc ctg aca cct gag gac tct gcc gtc tat tac tgt 288
 Met Gln Leu Ser Ser Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

tca agt cgc ggc gtc agg ggc tct atg gac tac tgg ggt caa gga acc 336
 Ser Ser Arg Gly Val Arg Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

tca gtc acc gtc tcc tca 354
 Ser Val Thr Val Ser Ser
 115

<210> 72
 <211> 324
 <212> DNA
 <213> Murine

<220>
 <221> CDS
 <222> (1)...(324)

<400> 72
 gat att cag atg acc cag act aca tcc tcc ctg tct gcc tct ctg gga 48
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly

1

5

10

15

gac aga gtc acc atc act tgc agg tca agt cag gac att agc aat ttt 96
 Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asp Ile Ser Asn Phe

20

25

30

tta aac tgg tat cag cag aaa cca gat gga act gtt aaa ctc ctg atc 144
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Ile
 35 40 45

tac tac aca tca aca tta cac tca gga gtc cca tca agg ttc agt ggc 192
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

agt ggg tct gga aca gat tat tct ctc acc att agc aac ctg gag caa 240
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

gaa gat att gcc act tac ttt tgc caa cag ggt aat acg ctt cct tgg 288
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

acg ttc ggt gga ggc acc aac ctg gaa atc aaa cgg 324
 Thr Phe Gly Gly Thr Asn Leu Glu Ile Lys Arg
 100 105

<210> 73

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/chimpanzee sequence

<400> 73

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asp Ile Ser Asn Phe			
20	25	30	
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile			
35	40	45	
Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly			
50	55	60	
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro			
65	70	75	80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp			
85	90	95	
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg			
100	105		

<210> 74
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> murine/chimpanzee sequence

<400> 74			
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr			
20	25	30	
Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile			
35	40	45	
Gly Glu Ile Leu Pro Arg Ser Gly Asn Thr Asn Tyr Asn Glu Lys Phe			
50	55	60	
Lys Gly Lys Ala Ser Phe Asn Ala Asp Thr Ser Thr Asn Ile Ala Tyr			
65	70	75	80
Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ser Ser Arg Gly Val Arg Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr			
100	105	110	

Leu Val Thr Val Ser Ser

115

<210> 75

<211> 360

<212> DNA

<213> Murine

<220>

<221> CDS

<222> (1)...(360)

<400> 75

caa gtt cag ctt caa cag cct ggg gct gag ctt gtg aag tct ggg gcc
 Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Ser Gly Ala
 1 5 10 15

48

tca gtg aag ctg tcc tgc aag gct tct ggc agt acc ttc acc agc tac
 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr
 20 25 30

96

tgg atg cac tgg gtg aag cag agg cct gga cga ggc ctt gag tgg att
 Trp Met His Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
 35 40 45

144

gga agg att gat cca aat agt ggt ggt act aag gat aat gag aag ttc
 Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe
 50 55 60

192

aag agc aag gcc aca ctg act gta gac aaa ccc tcc agc aca gcc tac
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr
 65 70 75 80

240

atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat tat tgt
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

288

100

gca aga gag acc tac tat gat tcc tcg ttt gct tac tgg ggc caa ggg 336
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

act ctg gtc act gtc tct gca gcc 360
 Thr Leu Val Thr Val Ser Ala Ala
 115 120

<210> 76
 <211> 336
 <212> DNA
 <213> Murine

<220>
 <221> CDS
 <222> (1) ... (336)

<400> 76 48
 gat att gtt atg act cag tct caa aaa ttc atg tcc aca tca gta gga
 Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15

gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96
 Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30

gta gcc tgg tat caa cag aaa cca ggg caa tct cct aaa gca ctg att 144
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
 35 40 45

. tac tcg gca tcc tac cgg tac agt gga gtc cct gat cgc ttc aca ggc 192
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc aat gtg cag tct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
 101

65

70

75

80

gaa gac ttg gca gag tat ttc tgt cag caa tat aac agc tat cct ctc
 Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu

85

90

95

acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgg gct gat gct gca
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala

100

105

110

288

336

<210> 77

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/chimpanzee sequence

<400> 77

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn

20

25

30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile

35

40

45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu

85

90

95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 78

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/chimpanzee sequence

<400> 78

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr
 20 25 30
 Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe
 50 55 60
 Lys Ser Lys Ala Thr Leu Asn Val Asp Lys Ser Thr Asn Ile Ala Tyr
 65 70 75 80
 Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Met Val Thr Val Ser
 115

<210> 79

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/human sequence

<400> 79

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr
 20 25 30

Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe
 50 55 60
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Met Val Thr Val Ser Ala
 115

<210> 80

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/human sequence

<400> 80

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
 35 40 45
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Thr
 100

<210> 81
<211> 11
<212> PRT
<213> Pan troglodytes

<400> 81
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 82
<211> 11
<212> PRT
<213> Pan troglodytes

<400> 82
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 83
<211> 11
<212> PRT
<213> Pan troglodytes

<400> 83
Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 84
<211> 11
<212> PRT
<213> Pan troglodytes

<400> 84
Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser
1 5 10

<210> 85

<211> 11
<212> PRT
<213> Pan troglodytes

<400> 85
Trp Gly Arg Gly Ile Leu Val Ile Val Ser Ser
1 5 10

<210> 86
<211> 11
<212> PRT
<213> Pan troglodytes

<400> 86
Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
1 5 10

<210> 87
<211> 11
<212> PRT
<213> Pan troglodytes

<400> 87
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
1 5 10

<210> 88
<211> 11
<212> PRT
<213> Macaca cynomolgus

<400> 88
Trp Gly Arg Gly Val Leu Val Thr Val Ser Ser
1 5 10

<210> 89
<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 89

Trp Gly Gln Gly Val Gln Val Thr Val Ser Ser

1 5 10

<210> 90

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 90

Trp Gly Pro Gly Val Met Val Thr Val Ser Ser

1 5 10

<210> 91

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 91

Trp Gly Arg Gly Leu Leu Val Thr Val Ser Ser

1 5 10

<210> 92

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 92

Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser

1 5 10

<210> 93

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 93

Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser
1 5 10

<210> 94

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 94

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
1 5 10

<210> 95

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 95

Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
1 5 10

<210> 96

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 96

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
1 5 10

<210> 97

<211> 11

<212> PRT

<213> Pan troglodytes

<400> 97

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg

1

5

10

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